

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:16:48 ; Search time 2680.05 Seconds
(without alignments)
11304.265 Million cell updates/sec

Title: US-09-807-933B-12
Perfect score: 1041
Sequence: 1 atgaagtctccatcatgcg.....ctggttcgagcgcaagtaa 1041

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :					GenEmbl:*				
1:	gb_ba:*	2:	gb_htg:*	3:	gb_in:*	4:	gb_om:*	5:	gb_ov:*
6:	gb_pat:*	7:	gb_ph:*	8:	gb_pl:*	9:	gb_pr:*	10:	gb_ro:*
11:	gb_sts:*	12:	gb_sy:*	13:	gb_un:*	14:	gb_vi:*	15:	em_ba:*
16:	em_fun:*	17:	em_hum:*	18:	em_in:*	19:	em_mu:*	20:	em_om:*
21:	em_or:*	22:	em_ov:*	23:	em_pat:*	24:	em_ph:*	25:	em_pl:*
26:	em_ro:*	27:	em_sts:*	28:	em_un:*	29:	em_vi:*	30:	em_htg_hum:*
31:	em_htg_inv:*	32:	em_htg_other:*	33:	em_htg_mus:*	34:	em_htg_pln:*	35:	em_htg_rod:*
36:	em_htg_man:*	37:	em_htg_vrt:*	38:	em_sy:*	39:	em_htgo_hum:*	40:	em_htgo_mus:*
41:	em_htgo_other:*								

ALIGNMENTS

RESULT 1				A68072				Sequence 67 from Patent WO9743409.				919 bp				DNA				linear				PAT 05-MAY-1999			
A68072				LOCUS				Sequence 67 from Patent WO9743409.																			
DEFINITION				A68072				A68072.1				GI:4756872															
ACCESSION				A68072				A68072.1				GI:4756872															
VERSION				A68072.1				GI:4756872				GI:4756872															
KEYWORDS				unidentified.				unidentified.				unclassified.															
SOURCE				unclassified.				unclassified.				unclassified.															
ORGANISM				unclassified.				unclassified.				unclassified.															
REFERENCE				1 (bases 1 to 919)				1 (bases 1 to 919)				1 (bases 1 to 919)															
AUTHORS				Dalboege,H., Diderichsen,B., Sandal,T. and Kauppinen,S.				Dalboege,H., Diderichsen,B., Sandal,T. and Kauppinen,S.				Dalboege,H., Diderichsen,B., Sandal,T. and Kauppinen,S.															
TITLE				METHOD OF PROVIDING NOVEL DNA SEQUENCES				METHOD OF PROVIDING NOVEL DNA SEQUENCES				METHOD OF PROVIDING NOVEL DNA SEQUENCES															
JOURNAL				Patent: WO 9743409-A 67 20-NOV-1997;				Patent: WO 9743409-A 67 20-NOV-1997;				Patent: WO 9743409-A 67 20-NOV-1997;															
				NOVONORDISK AS (DK)				NOVONORDISK AS (DK)				NOVONORDISK AS (DK)															

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 919)
TITLE	Dalb.o slashed.ge.H., Sandal,T., Kauppinen,M.Sakari. and Diderichsen,Bslashedrge.
JOURNAL	Method of providing a hybrid polypeptide exhibiting an activity of interest
FEATURES	Patent: US 6270968-A 67 07-AUG-2001;
source	Location/Qualifiers
BASE COUNT	165 a 325 c 256 g 173 t
ORIGIN	1..919
	/organism="unknown"
Query Match	23.2%; Score 241; DB 6; Length 919;
Best Local Similarity	63.1%; Pred.No. 9.2e-35;
Matches	392; Conservative 0; Mismatches 220; Indels 9; Gaps 176
QY	417 TGCGCTTCTTGGAAACGGTCCGCACTACCCGCTACTGGGATGTGTCGAAGCCCTCTTGCGC 476
Db	61 TGCTTTTCGCTGCTGATGCGCAGGTCCACGAGTACTGGGATTGTTGTAAGCCCTCTTGCTC 120
QY	477 CTGGGCGGAAGAGCTTCTGTAAGCTGCTACTCACCTGTGCGCAAGGATGTGTGTCAG 536
Db	121 CTGGGCGCAAGAGCTTCGGTCAAGCCCGCTCTACCTTGCACGAAGACGACACCC 180
QY	537 CCGTCTCGGTTCCGATGTCCAGAGCGGTTCGCTGGCGGCGAGCCCTACATGTGCAATGA 596
Db	181 CATCTCCGACGCCAAAGCCGTGAGCGGTTGCAACGGCGGCACCTTCCTACACCTGCAGCAA 240
QY	597 CAACGAGCCCTGGGTTGCTCAATCAGCAGCTTCGCTACGGTTTCGCTGCTGCCAGTCTCGG 656
Db	241 CAATCCCCGTGGGCTGTCAACGACAACTCGGCTATGGCTTTGCGCGTACCAAGCTCTC 300
QY	657 TAGCGCGGTGCTCTGCAATCTTGCTCGCGCTGTTCAGAGCTTACCTTTCACCAACACTGC 716
Db	301 TGGAGGCTCCGAGTCCAGCTGGTGTGCTTGCTAGCTCTCACCTTTACGACTGGCCC 360
QY	717 TGTGCTGGCAAGAGTTGTTGCTGCAGGTCAACAACCCGGTGAATGATCTCAGCACAA 776
Db	361 CGTGAAGGGCAAGACCATGTTGCTACAGTCCACCAACACCGGAGGCGATCTCGGCGAGAA 420
QY	777 CCACTTTGATTTCAGATGCCGGCGGTGTGTCGGCTACTTCAAAGGCTGCCAGTCCCA 836
Db	421 CCACTTCGATCTCCAGATGCCGGCGGCGGTGTGCGCATCTTTGACGGCTGCAGCTCCA 480
QY	837 GTGGAAACAACAACCGATGGCTGGGTGTCCTGATATGGCGGTATTAGCTCTATTTCAGA 896
Db	481 GTGG-----GGTGGGCTCCGGCGGTCTCAGTACGGCGGATCTCGTCGCGAAGCGA 531
QY	897 GTGCGCAGAGCTTCTTACCAGTTGCAGGCTGGTTCGAGTGGAGATTCCGATGGTTCAA 956
Db	532 CTGCGCAGAGTTCCCGAGCTGCTCAAGGACGGCTGCTACTGGCGCTACCACTGGTTCAA 591
QY	957 GAACGCTGCAACCCAGAGGTCACTTCAAGGCTGTTACTTGGCCCTGCCAGATCATTCG 1016
Db	592 GAACGCCGCAATCCGAGCTTTCAGTTCCGTCAGGTCCAGTGGCCAGCCGAGCTCGTCGC 651
QY	1017 CAAGACTGGTTGGAGGGCAA 1037
Db	652 TCGCACCGGATCCGCGGCAA 672
RESULT 3	
AR094309	
LOCUS	AR094309 1423 bp DNA linear PAT 08-SEP-2000
DEFINITION	Sequence 9 from patent US 6001639.
ACCESSION	AR094309
VERSION	AR094309.1 GI:10021117
KEYWORDS	Unknown.
SOURCE	

RESULT	3
AR094309	
LOCUS	AF094309
DEFINITION	Sequence 9 from patent US 6001659.
ACCESSION	AR094309
VERSION	AR094309.1
KEYWORDS	GI:10021117
SOURCE	Unknown.
	DNA
	linear
	PAT 08-SEP-2000

Wed Jun 18 17:55:08 2003

```
QY 1021 ACTGGTTCCGAGCG 1034
Db 731 AGTGGATGCAAGCG 744

RESULT 5
A21795 1473 bp mRNA linear PAT 20-SEP-1995
LOCUS F. oxysporum mRNA for endonuclease component.
DEFINITION
ACCESSION A21795
VERSION A21795.1 GI:1246874
KEYWORDS
SOURCE Fusarium oxysporum.
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
FEATURES
source Location/Qualifiers
1..1473
/organism="Fusarium oxysporum"
/strain="DSM 2672"
/db_xref="taxon:5507"
87..1227
/codon_start=1
/product="endonuclease"
/protein_id="CAA01575.1"
/db_xref="GI:1246875"
/translation="MRSYTLALAGPLAVSAASGSHSTRYWDCKPSCWSGKAIVN
APALTCDKNDFISNTNVAIVGCEGGSAYACTNYSWVAVNDLAYGFAATKISGSEA
SWCCACVALTFTTGPVKGMIVOSTNTGDLGDNHFDLMPGGVGIIDGCTSEFGK
ALGQAQGGTISRSECDSPYELLKDGCHWRFDWENADNPDFTFEOVQCPKALLDISG
CKRDDSSFPAPKVDTSASKPQSPSSAKKTSAAQAPOKTKDSAPVVKQSKTKPAA
QPEPTKPADKPDTPKVPATKPAATKPVQVNPVKTKTKVGRGTRGSCPAKTDATAKA
SVVPAYTQCGGSKSAYPNGLNACATGSKQKNEYYSQCVN"
BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN
Query Match 22.6%; Score 235.2; DB 6; Length 1473;
Best Local Similarity 63.8%; Pred. No. 1e-33; Indels 9; Gaps 2;
Matches 392; Conservative 0; Mismatches 213;
QY 424 TCTGGAACCGGTGCGCACTACCGCTACTGGGATGCTGCAAGCCCTCTTGGCGCTGGAC 483
Db 151 TCTGGAAGCGGTCACTCTACTCGATCTGGGATGCTGCAAGCCCTCTTGGGAGC 210
QY 484 GGAAGCGTCTGTAACTAAGCGGTGACTCACCCTGCTGCAAGCCCTCTTGGCGCTGGAC 543
Db 211 GGAAGCGTCTGTCAACGCCCTCTGCTTTAACTTGTGATAGAACGCAACCCCACTTC 270
QY 544 GGTTCGCATGTCAGAGCGGTG---CGTGGCGGCCAGGCTTACATGTGCAATGACAAC 600
Db 271 AACACCAATGCTGTCAACGGTTGTGAGGGTGGTGTCTGCTTATGCTTGCAACCACTAC 330
QY 601 CAGCCCTGGGTGTCAATGACGACCTTGCCTTACGGTTTGGTGTGCTGCTCGGTAGC 660
Db 331 TCTCCCTGGGCTGTCAACGATGAGCTTGCCTTACGCTTACGCTTACCAAGATCTCCGGT 390
QY 661 GCGGTGCTTGTGATCTTCTGCTGGGCTGTGTTACGAGCTTACCTTCAACCACTGCTGC 720
ORIGIN
Query Match 22.6%; Score 235.2; DB 6; Length 1473;
Best Local Similarity 63.8%; Pred. No. 1e-33; Indels 9; Gaps 2;
Matches 392; Conservative 0; Mismatches 213;
QY 424 TCTGGAACCGGTGCGCACTACCGCTACTGGGATGCTGCAAGCCCTCTTGGCGCTGGAC 483
Db 151 TCTGGAAGCGGTCACTCTACTCGATCTGGGATGCTGCAAGCCCTCTTGGGAGC 210
QY 484 GGAAGCGTCTGTAACTAAGCGGTGACTCACCCTGCTGCAAGCCCTCTTGGCGCTGGAC 543
Db 211 GGAAGCGTCTGTCAACGCCCTCTGCTTTAACTTGTGATAGAACGCAACCCCACTTC 270
QY 544 GGTTCGCATGTCAGAGCGGTG---CGTGGCGGCCAGGCTTACATGTGCAATGACAAC 600
Db 271 AACACCAATGCTGTCAACGGTTGTGAGGGTGGTGTCTGCTTATGCTTGCAACCACTAC 330
QY 601 CAGCCCTGGGTGTCAATGACGACCTTGCCTTACGGTTTGGTGTGCTGCTCGGTAGC 660
Db 331 TCTCCCTGGGCTGTCAACGATGAGCTTGCCTTACGCTTACGCTTACCAAGATCTCCGGT 390
QY 661 GCGGTGCTTGTGATCTTCTGCTGGGCTGTGTTACGAGCTTACCTTCAACCACTGCTGC 720
ORIGIN
Query Match 22.6%; Score 235.2; DB 6; Length 1473;
Best Local Similarity 63.8%; Pred. No. 1e-33; Indels 9; Gaps 2;
Matches 392; Conservative 0; Mismatches 213;
QY 424 TCTGGAACCGGTGCGCACTACCGCTACTGGGATGCTGCAAGCCCTCTTGGCGCTGGAC 483
Db 151 TCTGGAAGCGGTCACTCTACTCGATCTGGGATGCTGCAAGCCCTCTTGGGAGC 210
QY 484 GGAAGCGTCTGTAACTAAGCGGTGACTCACCCTGCTGCAAGCCCTCTTGGCGCTGGAC 543
Db 211 GGAAGCGTCTGTCAACGCCCTCTGCTTTAACTTGTGATAGAACGCAACCCCACTTC 270
QY 544 GGTTCGCATGTCAGAGCGGTG---CGTGGCGGCCAGGCTTACATGTGCAATGACAAC 600
Db 271 AACACCAATGCTGTCAACGGTTGTGAGGGTGGTGTCTGCTTATGCTTGCAACCACTAC 330
QY 601 CAGCCCTGGGTGTCAATGACGACCTTGCCTTACGGTTTGGTGTGCTGCTCGGTAGC 660
Db 331 TCTCCCTGGGCTGTCAACGATGAGCTTGCCTTACGCTTACGCTTACCAAGATCTCCGGT 390
QY 661 GCGGTGCTTGTGATCTTCTGCTGGGCTGTGTTACGAGCTTACCTTCAACCACTGCTGC 720
```

Db 391 GGCTCCGAGCCAGCTGGTCTGCTGTGCTATGCTTTTGACCTTACCACTGCCCCCGTC 450
 Qy 721 GCTGGCAAGAGTTTGTGTCAGGTCACCAACACCGGTGATGATCTCAGCAACCAACCAC 780
 Db 451 AAGGGCAAGAGATGATGCTCCAGTCCACCAACACTGGAGGTGATCTCGGCGCAACCAAC 510
 Qy 781 TTTGATTGTCAGATGCCCGCGGTGGTGTGCGGTACTTCAACGGCTGCCAGTCCCAAGTGG 840
 Db 511 TTGATCTCATGATGCCCGCGGTGGTGTGCGGTATCTTCGACGGCTGCACCTCTGAGT-- 568
 Qy 841 AACACCAACCAAGCTGGTGGGTGCTGCTATGCGGGTATTAGCTCTATTTCAGAGTGC 900
 Db 569 ----TCGGCAAGCTCTCGCGGTGCCAGTACGCGGGTATCTCTCCGAAACGGAATGT 624
 Qy 901 GACAAGCTTCTACCAAGCTTGCAGGCTGGTGTGCAAGTGGAGATTCGGATGGTTCAAGAAC 960
 Db 625 GATAGTACCCGAGCTTCTCAAGGACGGTGGTGCACCTGGCGATTCGACTGGTTGAGAAC 684
 Qy 961 GCTGACAACCAAGAGTCACTTCAAGGCTGTGTTACTTTGCCCTCCGAGATCATTTGCCAAG 1020
 Db 685 GCGGACAACCTGACTTCACTTTGAGCAGGTTTCAAGTGGCCCAAGGCTCTCTCTCGACATC 744
 Qy 1021 ACTGGTTGCGAGCG 1034
 Db 745 AGTGGATGCAAGCG 758

RESULT 7
 A23646
 LOCUS 1473 bp mRNA linear PAT 23-FEB-1995
 DEFINITION F. oxysporum endoglucanase gene.
 ACCESSION A23646
 VERSION A23646.1 GI:832892
 KEYWORDS Fusarium oxysporum.
 ORGANISM Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
 complex.
 1 (bases 1 to 1473)
 Convents,A.C., Busch,A. and Baek,A.C.
 Detergent compositions with high activity cellulase and quaternary
 ammonium compounds
 Patent: EP 0495554-A 3 22-JUL-1992;
 THE PROCTER & GAMBLE COMPANY
 LOCATION/Qualifiers
 1..1473
 /organism="Fusarium oxysporum"
 /strain="DSM 2672"
 /db_xref="taxon:5507"
 97..1227
 /codon_start=1
 /product="endoglucanase"
 /protein_id="CAA01684.1"
 /db_xref="GI:832893"
 /translation="MRSYTLALAGPLAVSAAGSGHSTRYWDCCPKSPCSWSGKAAVN
 APALTCNDKNPISTNNAVNGCGGSVACTNYSWAVNDELAAYGFAATKISGSEA
 SWCCACVALFTPTGPKGKMIQVSTNTGDLGNHFDLMPGGGVIGIDGCTSEFGK
 ALGGAQVGLSSRSECDYPELLKDGCHWRFDWFENADNPDFTFEQVQCPKALLDLSG
 CKRDDSSPFAKVDTSASPKQPSAKKTSAAQPKTKDSAPVVKSKTKPAA
 QPEPTKPADKPKVDTSASPKQPSAKKTSAAQPKTKDSAPVVKSKTKPAA
 SVVPAYVQCGSKSAYPNGNLACATGSKCKVQNEYYSQCPVN"
 BASE COUNT 343 a 453 c 337 g 340 t
 ORIGIN

Query Match 22.6%; Score 235.2; DB 6; Length 1473;
 Best Local Similarity 63.8%; Pred. No. 1e-33;
 Matches 392; Conservative 0; Mismatches 213; Indels 9; Gaps 2;
 Qy 424 TCTGGAACCGTGCACCTACCGCTACTGGATTGCTGCAAGCCCTTTCGGCTGGGAC 483
 Db 151 TCTGGAACCGTCACTCTACTCGATCTGGGATTGCTGCAAGCCCTTCTTCTCTGGAGC 210

Qy 484 GGAAAGGCTTCTGTAACGCTGTACTCACCTGTGCCAAGGATGGTGTACGCGCTCTC 543
 Db 211 GGAAAGGCTGTCTCAACGCCCTGCTTTTAACTTGTGATAAGAAACGCAACCCATTTCC 270
 Qy 544 GGTTCGGATGTCAGAGCGGTTG---CGTCGGCGGCCAGGCTCATATGTGCAATGACAAC 600
 Db 271 AACACCAATGCTGTCAACGGTTGTGAGGGTGGTGTCTCTTATGCTTGCACCAACTAC 330
 Qy 601 CAGCCCTGGTGTCAATGACGACCTTGTCTACGGTTTTCGCTGCTCCAGTCTCGGTAGC 660
 Db 331 TCTCCCTGGGCTGTCAACGATGAGCTTGTGCTACGGTTTTCGCTGCTACCAAGATCTCGGT 390
 Qy 661 GCGGTGCTCTGCAATTCGCTGCGGCTGTTCAGAGCTTACCTTCAACCAACACTGTGTC 720
 Db 391 GGTCCGAGCCAGCTGGTGTGCTGTCTATGCTTTTGACCTTTCACCACTGCCCGCTC 450
 Qy 721 GCTGGCAAGAGTTTGTCTCAGGTCAACCAACCGGTGATGATCTCAGCACCACCAACC 780
 Db 451 AAGGGCAAGAGATGATGCTCCAGTCCACCAACACTGAGAGGTGATCTCGGCGCAACACC 510
 Qy 781 TTTGATTGTCAGATGCCCGCGGTGGTGTGCGGTACTTCAACGGCTGCCAGTCCCAAGTGG 840
 Db 511 TTGATCTCATGATGCCCGCGGTGGTGTGCGGTATCTTCGACGGCTGCACCTCTGAGT-- 568
 Qy 841 AACACCAACCAAGTGGCTGCTGCTATGCGGCTATTAGCTCTATTTCAGAGTGC 900
 Db 569 ----TCGGCAAGCTCTCGCGGTGCCAGTACGCGGTATCTCTCCCGAAGCGAATGT 624
 Qy 901 GACAAGCTTCTACCAAGTGGTGGTGTGCAAGTGGAGATTCGGATGGTTCAAGAAC 960
 Db 625 GATAGTACCCGAGCTTCTCAAGGACGGTGGTGCACCTGGCGATTCGACTGGTTGAGAAC 684
 Qy 961 GCTGACAACCAAGAGTCACTTCAAGGCTGTGTTACTTTGCCCTCCGAGATCATTTGCCAAG 1020
 Db 685 GCGGACAACCTGACTTCACTTTGAGCAGGTTTCAAGTGGCCCAAGGCTCTCTCTCGACATC 744
 Qy 1021 ACTGGTTGCGAGCG 1034
 Db 745 AGTGGATGCAAGCG 758
 RESULT 8
 A23955
 LOCUS 1473 bp DNA linear PAT 01-MAR-1995
 DEFINITION Endoglucanase gene.
 ACCESSION A23955
 VERSION A23955.1 GI:832896
 KEYWORDS Fusarium oxysporum.
 ORGANISM Fusarium oxysporum
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
 complex.
 1 (bases 1 to 1473)
 Baek,A.C., Busch,A. and Ceulemans,R.A.A.
 Compact detergent compositions with high activity cellulase
 Patent: EP 0495257-A 3 22-JUL-1992;
 THE PROCTER & GAMBLE COMPANY
 LOCATION/Qualifiers
 1..1473
 /organism="Fusarium oxysporum"
 /db_xref="taxon:5507"
 97..1227
 /codon_start=1
 /product="endoglucanase"
 /protein_id="CAA01697.1"
 /db_xref="GI:832897"
 /translation="MRSYTLALAGPLAVSAAGSGHSTRYWDCCPKSPCSWSGKAAVN
 APALTCNDKNPISTNNAVNGCGGSVACTNYSWAVNDELAAYGFAATKISGSEA
 SWCCACVALFTPTGPKGKMIQVSTNTGDLGNHFDLMPGGGVIGIDGCTSEFGK
 ALGGAQVGLSSRSECDYPELLKDGCHWRFDWFENADNPDFTFEQVQCPKALLDLSG
 CKRDDSSPFAKVDTSASPKQPSAKKTSAAQPKTKDSAPVVKSKTKPAA
 QPEPTKPADKPKVDTSASPKQPSAKKTSAAQPKTKDSAPVVKSKTKPAA
 QPEPTKPADKPKVDTSASPKQPSAKKTSAAQPKTKDSAPVVKSKTKPAA
 SVVPAYVQCGSKSAYPNGNLACATGSKCKVQNEYYSQCPVN"
 BASE COUNT 343 a 453 c 337 g 340 t
 ORIGIN

BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN SVVPAYQCGGSKSAYPNGLACATGSKCVKQNEYYSQCVPN"

Query Match 22.6%; Score 235.2; DB 6; Length 1473;
Best Local Similarity 63.8%; Pred. No. 1e-33;
Matches 392; Conservative 0; Mismatches 213; Indels 9; Gaps 2;
QY 424 TCTGGAACCGTCCGCACTACCGCTACTGGGATTGCTGCAAGCCCTCTTGGCGCTGGAC 483
DB 151 TCTGGAAGCGTCACTTACTCGATATGGATTGCTGCAAGCTTCTTGGCTTTGGAGC 210
QY 484 GGAAGGCTTCTGTAACTAAGCCTGTACTCACTGTGCCAAGGATGCTGACCGCTCTC 543
DB 211 GGAAGGCTGTCTCAAGCCCTGCTTTAACTTGTGATAAGAACGACCAACCCATTTC 270
QY 544 GGTTCAGATGCCAGAGCGGTG---CGTCGGCGGCCAGGCTACATGTCATGACAAC 600
DB 271 AACACCAATGCTGTCAACCGGTTGTAGGGGTGTGGTGTCTGCTTATGCTTGCAACCACTAC 330
QY 601 CAGCCCTGGGTTGTCAATGACGACCTTGCCTACCGTTTTCGCTGCTGCGCAGTCTCGGTAGC 660
DB 331 TCTCCCTGGGCTGTCAACGATGAGCTTGCCTACGCTTTCGCTGCTACTCAAGATCTCGGT 390
QY 661 GCCGGTGCCTGTGATCTGCTGCGGCTGTTAAGAGCTTACCTTCAACCAACACTGCTGTC 720
DB 391 GGCTCCGAGGCGAGCTGTGTGCTGTGCTTATGCTTTGACCTTCAACCACTGCGCCCGTC 450
QY 721 GCTGGCAAGAGTTGTGCTCAGGTACCAACACCGGTGATGATCTCAGCAACCAAC 780
DB 451 AAGGGCAAGAGATGATGCTCCAGTCCACCAACTGGAGGTGATCTCGGCGCAACCA 510
QY 781 TTTGATTGAGATGCCCGGCTGTGCTGCTTCAAGGCTTCCAGCTGCCAGTCCAGTGG 840
DB 511 TTGATCTCATGATGCCCGGCTGTGCTCGGTATCTTCGAGGCTGCACCTCTGAGT-- 568
QY 841 AACACCAACCGATGGGCTGCTGCTATATGGCGGTATAGCTTATTTAGAGTGC 900
DB 569 ----TCGGCAAGGCTCTCGGCGGTGCCAGTACGCGGCTATCTCTCCGAAAGCGAATGT 624
QY 901 GACAAGCTTCTACCCAGTTGTCAGGCTGTTGCAAGTGGAGATTCGGATGTTCAAGAAC 960
DB 625 GATAGTACCCCGAGCTTCTCAAGGACGGTTGCCATCGGATTCGACTGGTTCGAGAAC 684
QY 961 GCTGACAAACCGAGAGTCACTTCAAGGCTGTTACTTGGCCCTGCCGAGATCAITGGCAAG 1020
DB 685 GCCGACAAACCTGACTTCACTTTGAGCAGGTTCAGTGCCTCCCAAGGCTCTCTCGACATC 744
QY 1021 ACTGGTTGCGAGCG 1034
DB 745 AGTGGATGCAAGCG 758

RESULT 9
A23959
LOCUS A23959 1473 bp DNA linear PAT 01-MAR-1995
DEFINITION Endoglucanase gene.
ACCESSION A23959
VERSION A23959.1 GI:832900
KEYWORDS Fusarium oxysporum.
SOURCE Fusarium oxysporum
ORGANISM Fusarium oxysporum
Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
REFERENCE 1 (bases 1 to 1473)
AUTHORS McCorquodale, F. and Busch, A.
TITLE Dye transfer inhibiting compositions
JOURNAL Patent: EP 0540784-A 3 12-MAY-1993;
THE PROCTER & GAMBLE COMPANY
FEATURES Location/Qualifiers
source 1..1473
/organism="Fusarium oxysporum"

/db_xref="taxon:5507"
97..1227
/codon_start=1
/product="endoglucanase"
/protein_id="CAA01699.1"
/db_xref="GI:832901"
/translation="MRSYTLALAGPLAVSAASGSGHSTRYWDCKPSCSWGKAAYN
APALTCDKNDNPISTNAVNGEGGSAVACTNYSPWAVDELAYGFAATKISGSEA
SWCCAYALTFTTGPVKKKMIVQSTNTGDLNDHFDLMVPGGVGIPDCTSEFGK
ALGGAQYGGISRSSECDSSYPELLKDGCHWRFDWFENADNPDFTFEVQCPKALLDLSG
QRDDSSPPAPKVDTSASKPQSPSSAKTTSAAARAAQPKTKDSAPVQKSKTKPAA
QREPTKADKPQTDKPAATPAATPVNPKPTTKVRGTGRTGSCFPAKTUATAKA
SVVPAYQCGGSKSAYPNGLACATGSKCVKQNEYYSQCVPN"
BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN

Query Match 22.6%; Score 235.2; DB 6; Length 1473;
Best Local Similarity 63.8%; Pred. No. 1e-33;
Matches 392; Conservative 0; Mismatches 213; Indels 9; Gaps 2;
QY 424 TCTGGAACCGTCCGCACTACCGCTACTGGGATTGCTGCAAGCCCTCTTGGCGCTGGAC 483
DB 151 TCTGGAAGCGTCACTTACTCGATATGGATTGCTGCAAGCTTCTTGGCTTTGGAGC 210
QY 484 GGAAGGCTTCTGTAACTAAGCCTGTACTCACTGTGCCAAGGATGCTGACCGCTCTC 543
DB 211 GGAAGGCTGTCTCAAGCCCTGCTTTAACTTGTGATAAGAACGACCAACCCATTTC 270
QY 544 GGTTCAGATGCCAGAGCGGTG---CGTCGGCGGCCAGGCTACATGTCATGACAAC 600
DB 271 AACACCAATGCTGTCAACCGGTTGTAGGGGTGTGGTGTCTGCTTATGCTTGCAACCACTAC 330
QY 601 CAGCCCTGGGTTGTCAATGACGACCTTGCCTACCGTTTTCGCTGCTGCGCAGTCTCGGTAGC 660
DB 331 TCTCCCTGGGCTGTCAACGATGAGCTTGCCTACGCTTTCGCTGCTACTCAAGATCTCGGT 390
QY 661 GCCGGTGCCTGTGATCTGCTGCGGCTGTGAGAGCTTACCTTCAACCAACACTGCTGTC 720
DB 391 GGCTCCGAGGCGAGCTGTGCTGCTTATGCTTTGACCTTCAACCACTGCGCCCGTC 450
QY 721 GCTGGCAAGAGTTGTGCTCAGGTACCAACACCGGTGATGATCTCAGCAACCAAC 780
DB 451 AAGGGCAAGAGATGATGCTCCAGTCCACCAACTGGAGGTGATCTCGGCGCAACCA 510
QY 781 TTTGATTGAGATGCCCGGCTGTGCTGCTTCAAGGCTTCCAGCTGCCAGTCCAGTGG 840
DB 511 TTGATCTCATGATGCCCGGCTGTGCTCGGTATCTTCGAGGCTGCACCTCTGAGT-- 568
QY 841 AACACCAACCGATGGGCTGCTGCTATATGGCGGTATAGCTTATTTAGAGTGC 900
DB 569 ----TCGGCAAGGCTCTCGGCGGTGCCAGTACGCGGCTATCTCTCCGAAAGCGAATGT 624
QY 901 GACAAGCTTCTACCCAGTTGTCAGGCTGTTGCAAGTGGAGATTCGGATGTTCAAGAAC 960
DB 625 GATAGTACCCCGAGCTTCTCAAGGACGGTTGCCATCGGATTCGACTGGTTCGAGAAC 684
QY 961 GCTGACAAACCGAGAGTCACTTCAAGGCTGTTACTTGGCCCTGCCGAGATCAITGGCAAG 1020
DB 685 GCCGACAAACCTGACTTCACTTTGAGCAGGTTCAGTGCCTCCCAAGGCTCTCTCGACATC 744
QY 1021 ACTGGTTGCGAGCG 1034
DB 745 AGTGGATGCAAGCG 758

RESULT 10
A41660
LOCUS A41660 1473 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 3 from Patent EP0633311.
ACCESSION A41660
VERSION A41660.1 GI:2297285
KEYWORDS unidentifed.
SOURCE


```
complex.
REFERENCE 1 (bases 1 to 1473)
AUTHORS Gurete,R., Moller,M.J., Martin,S. and Ananto,P.S.
TITLE Cellulase preparation comprising endoglucanase
JOURNAL Patent: JP 2000217593-A 2 08-AUG-2000;
COMMENT NOVO NORDISK A/S
OS Fusarium oxysporum
PN JP 2000217593-A/2
PD 08-AUG-2000
PF 22-DEC-1999 JP 1999365341
PR 09-MAY-1990 DK 1159/90,22-APR-1991 DK 0736/91 PI
RASMUSSEN GURETE,MIKKJELSEN JAN MOLLER,SCHREIN MARTIN, PI PATKUL
SHAMKANTO ANANTO
PC C12N15/09,C11D3/386,C12N1/15,C12N1/19,C12N9/42,C1293/04, PC
D06M16/00//
PC D21H11/20, (C12N9/42,C12R1:645),C12N15/00
CC
FH Key Location/Qualifiers
FT CDS (97). .(1224).
FEATURES
source 1. .1473
Location/Qualifiers
/organism="Fusarium oxysporum"
/db_xref="taxon:5507"
BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN
Query Match 22.6%; Score 235.2; DB 6; Length 1473;
Best Local Similarity 63.8%; Pred. No.1e-33;
Matches 392; Conservative 0; Mismatches 213; Indels 9; Gaps 2;
QY 424 TCTGGAAACGCTCGACATACCCGCTACTGGGATTGCTGCAAGCCCTCTTGGCGCTGGAC 483
Db 151 TCTGGAAAGCGTCACTCTACTCGATACGGGATGCTGCAAGCCCTCTTGGCTCTGGAGC 210
QY 484 GGAAGGCTTCTGTAACCTTAAGCCTGTACTCACCCTGTGCAAGGATGGTGCAGCCGCTC 543
Db 211 GGAAGGCTGCTGTCAACGCCCTGTCTTAACTTGTGATAGAACACACACCCATTCC 270
QY 544 GGTTCGATGTCAGAGCGGTG--CGTCGGCGGCCAGCCCTACATGTGCAATGACAAC 600
Db 271 AACACCAATGCTGTCAACGGTGTGAGGGTGTGCTGCTATGATAGAACACCACTAC 330
QY 601 CAGCCCTGGGTGTCAATGACGACCTTGCCTACGGTTGCTGCTGCGATCTCGGTAGC 660
Db 331 TCTCCCTGGGCTGTCAACGATGAGCTTGCCTACGGTTTGGCTGTACCAAGATCTCCGGT 390
QY 661 GCCGGTGCCTGTGATCTGCTGCGGCTGTACAGGCTTACCTTCACCAACACTGCTGTC 720
Db 391 GGCTCCGAGGCAGCTGGTGTGCTGTGCTGTATGCTTTGACCTTCACCACTGGCCCGTC 450
QY 721 GCTGGCAAGAGTTGTGCTCAGGTCAACCAACCGGTGATGATCTCAGCAACCAAC 780
Db 451 AAGGCAAGAGATGATGCTCCAGTCACCAACACTGGAGTGATCTCGGCGACCAACC 510
QY 781 TTTGATTTGCAAGTCCCGCGGTGTCTGGCTACTTCAACGCTGCCAGTCCAGTGG 840
Db 511 TTGATCTCATGATGCGCGGGGGTGTGCTGCTGATCTTCGACGCTGCACCTCTGAGT-- 568-
QY 841 AACACCAACACCGATGGCTGGGGTGTGCTGCTATGGCGGTATTTAGCTCTATTTTCAGAGTGC 900
Db 569 ----TCGGCAAGGCTCTCGCGGTGCGCAGTACGCGGTATCTCTCCGAGCGGATGT 624
QY 901 GACAAGCTTCTACCGATTGCAAGCTGGTGTGCAAGTGGAGATTCGATGGTTCAAGAAC 960
Db 625 GATAGCTACCCCGAGCTTCTCAAGGCGGTGGCCACTGGCGATTTCGACTGGTTGAGAAC 684
QY 961 GCTCACAAACCCAGAGGTCACTTCAAGGCTGTCTTACTTTCCTGCGGTGCGAGATTCATGCCAAG 1020
Db 685 GCCGACAACTTACTTACCTTTGACAGGTTGAGTTCAGTTCGCGCCCAAGGCTCTCTCGACATC 744
QY 1021 ACTGGTTCCGAGCG 1034
Db 745 AGTGGATGCAAGCG 758
```

```
RESULT 13
LOCUS BD010853 1473 bp DNA linear PAT 31-JAN-2002
DEFINITION Cellulase preparation containing endoglucanase.
ACCESSION BD010853
VERSION BD010853.1 GI:18639226
KEYWORDS JP 2001057894-A/2.
SOURCE Fusarium oxysporum.
ORGANISM Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
REFERENCE 1 (bases 1 to 1473)
AUTHORS Rasmussen,G., Mikkelsen,J.M., Schilein,M., Patkar,S.A., Hagen,F.,
Miland,H.K. and Hallstøp,S.
TITLE Cellulase preparation containing endoglucanase
JOURNAL Patent: JP 2001057894-A 2 06-MAR-2001;
COMMENT NOVO NORDISK AS
OS Fusarium oxysporum
PN JP 2001057894-A/2
PD 06-MAR-2001
PF 06-JUL-2000 JP 2000205757
PR 09-MAY-1990 DK 1159/90,22-APR-1991 DK 0736/91 PI
GURETE RASMUSSEN,JAN MOLLER MIKKJELSEN,MARTIN SCHILEIN, PI
SHAMKANT ANANT PATKAR,FRED HAGEN,HJORT KARSTEN MILAND, PI SVEND
HALLSTØP
PC C12N15/09,C11D3/386,C12N1/15,C12N1/19,C12N9/24,D06M16/00// PC
(C12N15/09,C12R1:77), (C12N15/09,C12R1:645), (C12N9/24, PC
C12R1:865),
PC (C12N9/24,C12R1:885), (C12N9/24,C12R1:78), (C12N9/24,C12R1:69),
PC (C12N9/24,C12R1:685),C12N15/00, (C12N15/00,C12R1:77),
(C12N15/00, PC C12R1:645)
CC
FH Key Location/Qualifiers
FT CDS 97. .1224.
FEATURES
source 1. .1473
Location/Qualifiers
/organism="Fusarium oxysporum"
/db_xref="taxon:5507"
BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN
Query Match 22.6%; Score 235.2; DB 6; Length 1473;
Best Local Similarity 63.8%; Pred. No.1e-33;
Matches 392; Conservative 0; Mismatches 213; Indels 9; Gaps 2;
QY 424 TCTGGAAACGCTCGACATACCCGCTACTGGGATTGCTGCAAGCCCTCTTGGCGCTGGAC 483
Db 151 TCTGGAAAGCGTCACTCTACTCGATACGGGATGCTGCAAGCCCTCTTGGCTCTGGAGC 210
QY 484 GGAAGGCTTCTGTAACCTTAAGCCTGTACTCACCCTGTGCAAGGATGGTGCAGCCGCTC 543
Db 211 GGAAGGCTGCTGTCAACGCCCTGTCTTAACTTGTGATAGAACACACACCCATTCC 270
QY 544 GGTTCGATGTCAGAGCGGTG--CGTCGGCGGCCAGCCCTACATGTGCAATGACAAC 600
Db 271 AACACCAATGCTGTCAACGGTGTGAGGGTGTGCTGCTATGATAGAACACCACTAC 330
QY 601 CAGCCCTGGGTGTCAATGACGACCTTGCCTACGGTTGCTGCTGCGATCTCGGTAGC 660
Db 331 TCTCCCTGGGCTGTCAACGATGAGCTTGCCTACGGTTTGGCTGTACCAAGATCTCCGGT 390
QY 661 GCCGGTGCCTGTGATCTGCTGCGGCTGTACAGGCTTACCTTCACCAACACTGCTGTC 720
Db 391 GGCTCCGAGGCAGCTGGTGTGCTGTGCTGTATGCTTTGACCTTCACCACTGGCCCGTC 450
QY 721 GCTGGCAAGAGTTGTGCTCAGGTCAACCAACCGGTGATGATCTCAGCAACCAAC 780
Db 451 AAGGCAAGAGATGATGCTCCAGTCACCAACACTGGAGTGATCTCGGCGACCAACC 510
QY 781 TTTGATTTGCAAGTCCCGCGGTGTCTGGCTACTTCAACGCTGCCAGTCCAGTGG 840
Db 511 TTGATCTCATGATGCGCGGGGGTGTGCTGCTGATCTTCGACGCTGCACCTCTGAGT-- 568-
QY 841 AACACCAACACCGATGGCTGGGGTGTGCTGCTATGGCGGTATTTAGCTCTATTTTCAGAGTGC 900
Db 569 ----TCGGCAAGGCTCTCGCGGTGCGCAGTACGCGGTATCTCTCCGAGCGGATGT 624
QY 901 GACAAGCTTCTACCGATTGCAAGCTGGTGTGCAAGTGGAGATTCGATGGTTCAAGAAC 960
Db 625 GATAGCTACCCCGAGCTTCTCAAGGCGGTGGCCACTGGCGATTTCGACTGGTTGAGAAC 684
QY 961 GCTCACAAACCCAGAGGTCACTTCAAGGCTGTCTTACTTTCCTGCGGTGCGAGATTCATGCCAAG 1020
Db 685 GCCGACAACTTACTTACCTTTGACAGGTTGAGTTCAGTTCGCGCCCAAGGCTCTCTCGACATC 744
QY 1021 ACTGGTTCCGAGCG 1034
Db 745 AGTGGATGCAAGCG 758
```

Db 511 TTGGATCTCATGATGCCGCGGTGGTTCGGTATCTTCGACGGCTGCACCTCTGAGT-- 568
Qy 841 AACACCAACACCGATGGCTGGGTGCTCGCTATGCGGTATTAGCTCTATTTCCAGAGTGC 900
Db 569 ----TCGGCAAGGCTCTCGCGGTGCCAGTAGTACGGCGGTATCTCTCTCCCGAAGCGAATGT 624
Qy 901 GACAAGCTTCTTACCCAGTTGCAAGTGGTGTGCAAGTGGAGATTCGGATGGTTCAAGAAC 960
Db 625 GATAGCTACCCGAGCTTCTCAAGGACGGTTGCCACTGGCGATTTCGACTGGTTCCGAGAAC 684
Qy 961 GCTGACAAACCCAGAGTCACTTCAAGGCTGTGTACTTGGCCCTGCCGAGATCATTTGCCAAG 1020
Db 685 GCGGACAAACCTGACTTCACTTTGAGCAGGTTTCAGTGCCCAAGGCTCTCTCCGACATC 744
Qy 1021 ACTGGTTGGAGCG 1034
Db 745 AGTGGATGCAAGCG 758

RESULT 14
LOCUS I13885 1473 bp DNA linear PAT 26-SEP-1995
DEFINITION Sequence 3 from patent US 5443750.
ACCESSION I13885
VERSION I13885.1 GI:996365
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1473)
AUTHORS Convents, A., Busch, A. and Baek, A.C.
TITLE Detergent compositions with high activity cellulase and softening
JOURNAL Patent: US 5443750-A 3 22-AUG-1995;
FEATURES Location/Qualifiers
1..1473
BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN /organism="unknown"

Query Match 22.6%; Score 235.2; DB 6; Length 1473;
Best Local Similarity 63.8%; Pred. No. 1e-33;
Matches 392; Conservative 0; Mismatches 213; Indels 9; Gaps 2;
Qy 424 TCTGGAACGGTCGCACTACCCGCTACTGGATTGCTGCAAGCCCTTTGGCGCTGGAC 483
Db 151 TCTGGAAGCGGTCACTCTACTCGATATGGGATTGCTGCAAGCCTTTCTTGCTCTGGAGC 210
Qy 484 GGAAGGCTTCTGTAAGCTGTACTCACCTGTGCCAAGGATGGTGCAGCCGTCTC 543
Db 211 GGAAGGCTGCTGTCAAGCCCTGTCTTAACTTGTGATAGAACACCAACCCATTTC 270
Qy 544 GGTTCGATGTCCAGAGCGGTG---CGTCGGCGCCAGGCCCTACATGTGCAATGACAAC 600
Db 271 AACACCAATGCTGTCAACGGTTGTGAGGGTGTGGTCTTGTATGTGTCACCAACTAC 330
Qy 601 CAGCCCTGGGTTGTCAATGACGACCTTGCTACGGTTTCGGCTGCTGCCAGTCTCGGTAGC 660
Db 271 AACACCAATGCTGTCAAGCGTTGTGAGGGTGTGGTCTTGTCTTATGCTTGCAACCACTAC 330
Qy 601 CAGCCCTGGGTTGTCAATGACGACCTTGCTACGGTTTCGGCTGCTGCCAGTCTCGGTAGC 660
Db 331 TCTCCCTGGGCTGTCAACGATGAGCTTGCCTACGGTTTCGGCTGCTACCAAGATCTCCGGT 390
Qy 661 GCGGCTGCTCTGCTATTCGCTGGCTGTTACGAGCTTACCTTCCACCAACCTGCTGTC 720
Db 391 GGTTCGAGCCAGCTGGTGTGCTGTGCTTGTATGCTTTGACCTTACCACTGCCCGCGTC 450
Qy 721 GCTGGCAAGAGTTTGTGCTCAAGTCAACCAACCGGTGATGATCTCAGACCAACCAAC 780
Db 451 AAGGGCAAGAGATGATGCTCCAGTCCACCAACACTGGAGGTGATCTCGGCGCAACCAAC 510
Qy 781 TTTGATTTGAGATGCCCGCGGTGTGCTCGGCTACTTCAAGCTGCGGATTTAGCTCTATTTCCAGAGTGC 840
Db 511 TTGGATCTCATGATGCCGCGGTGGTTCGGTATCTTCGACGGCTGCACCTCTGAGT-- 568

Qy 841 AACACCAACACCGATGGCTGGGTGCTCGCTATGCGGTATTAGCTCTATTTCCAGAGTGC 900
Db 569 ----TCGGCAAGGCTCTCGCGGTGCCAGTAGTACGGCGGTATCTCTCTCCCGAAGCGAATGT 624
Qy 901 GACAAGCTTCTTACCCAGTTGCAAGTGGTGTGCAAGTGGAGATTCGGATGGTTCAAGAAC 960
Db 625 GATAGCTACCCGAGCTTCTCAAGGACGGTTGCCACTGGCGATTTCGACTGGTTCCGAGAAC 684
Qy 961 GCTGACAAACCCAGAGTCACTTCAAGGCTGTGTACTTGGCCCTGCCGAGATCATTTGCCAAG 1020
Db 685 GCGGACAAACCTGACTTCACTTTGAGCAGGTTTCAGTGCCCAAGGCTCTCTCCGACATC 744
Qy 1021 ACTGGTTGGAGCG 1034
Db 745 AGTGGATGCAAGCG 758

RESULT 15
LOCUS I21317 1473 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 3 from patent US 5520838.
ACCESSION I21317
VERSION I21317.1 GI:1601671
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1473)
AUTHORS Baek, A.C., Ceulemans, R.A. and Busch, A.
TITLE Compact detergent compositions with high activity cellulase
JOURNAL Patent: US 5520838-A 3 28-MAY-1996;
FEATURES Location/Qualifiers
1..1473
BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN /organism="unknown"

Query Match 22.6%; Score 235.2; DB 6; Length 1473;
Best Local Similarity 63.8%; Pred. No. 1e-33;
Matches 392; Conservative 0; Mismatches 213; Indels 9; Gaps 2;
Qy 424 TCTGGAACGGTCGCACTACCCGCTACTGGATTGCTGCAAGCCCTTTGGCGCTGGAC 483
Db 151 TCTGGAAGCGGTCACTCTACTCGATATGGGATTGCTGCAAGCCTTTCTTGCTCTGGAGC 210
Qy 484 GGAAGGCTTCTGTAAGCTGTACTCACCTGTGCCAAGGATGGTGCAGCCGTCTC 543
Db 211 GGAAGGCTGCTGTCAAGCCCTGTCTTAACTTGTGATAGAACACCAACCCCATTTTC 270
Qy 544 GGTTCGATGTCCAGAGCGGTG---CGTCGGCGCCAGGCCCTACATGTGCAATGACAAC 600
Db 271 AACACCAATGCTGTCAACGGTTGTGAGGGTGTGGTCTTGTATGTGTCACCAACTAC 330
Qy 601 CAGCCCTGGGTTGTCAATGACGACCTTGCTACGGTTTCGGCTGCTGCCAGTCTCGGTAGC 660
Db 331 TCTCCCTGGGCTGTCAACGATGAGCTTGCCTACGGTTTCGGCTGCTACCAAGATCTCCGGT 390
Qy 661 GCGGCTGCTCTGCTATTCGCTGGCTGTGTAGGAGCTTACCTTCCACCAACCTGCTGTC 720
Db 391 GGTTCGAGCCAGCTGGTGTGCTGTGCTTGTATGCTTTGACCTTACCACTGCCCGCGTC 450
Qy 721 GCTGGCAAGAGTTTGTGCTCAAGTCAACCAACCGGTGATGATCTCAGACCAACCAAC 780
Db 451 AAGGGCAAGAGATGATGCTCCAGTCCACCAACACTGGAGGTGATCTCGGCGCAACCAAC 510
Qy 781 TTTGATTTGAGATGCCCGCGGTGTGCTCGGCTACTTCAAGCTGCGGATTTAGCTCTATTTCCAGAGTGC 840
Db 511 TTGGATCTCATGATGCCGCGGTGGTTCGGTATCTTCGACGGCTGCACCTCTGAGT-- 568
Qy 841 AACACCAACACCGATGGCTGGGTGCTCGCTATGCGGATTTAGCTCTATTTCCAGAGTGC 900
Db 569 ----TCGGCAAGGCTCTCGCGGTGCCAGTAGTACGGCGGTATCTCTCTCCCGAAGCGAATGT 624

